Supplemental Material S2

Figure S2. To test the effect of quality filtering by Usearch with different maximal error rates ranging between 0.04 and 0.08 on the consensus accuracy, we took the Pacbio generated consensus sequences as control and used local blast to assess the similarity values of the four specimens 16384, 16404, 16481, 16483. The test was done with the full-length sequences obtained from the TR-PCR. The quality drop at the most stringent filtering (0.04) that is seen in 3 of 4 cases, is likely due to the strong reduction in sequences that passed the filtering (see Table S2). There was no difference in consensus accuracy/similarity between 0.06 and 0.08 as filtering cutoff.
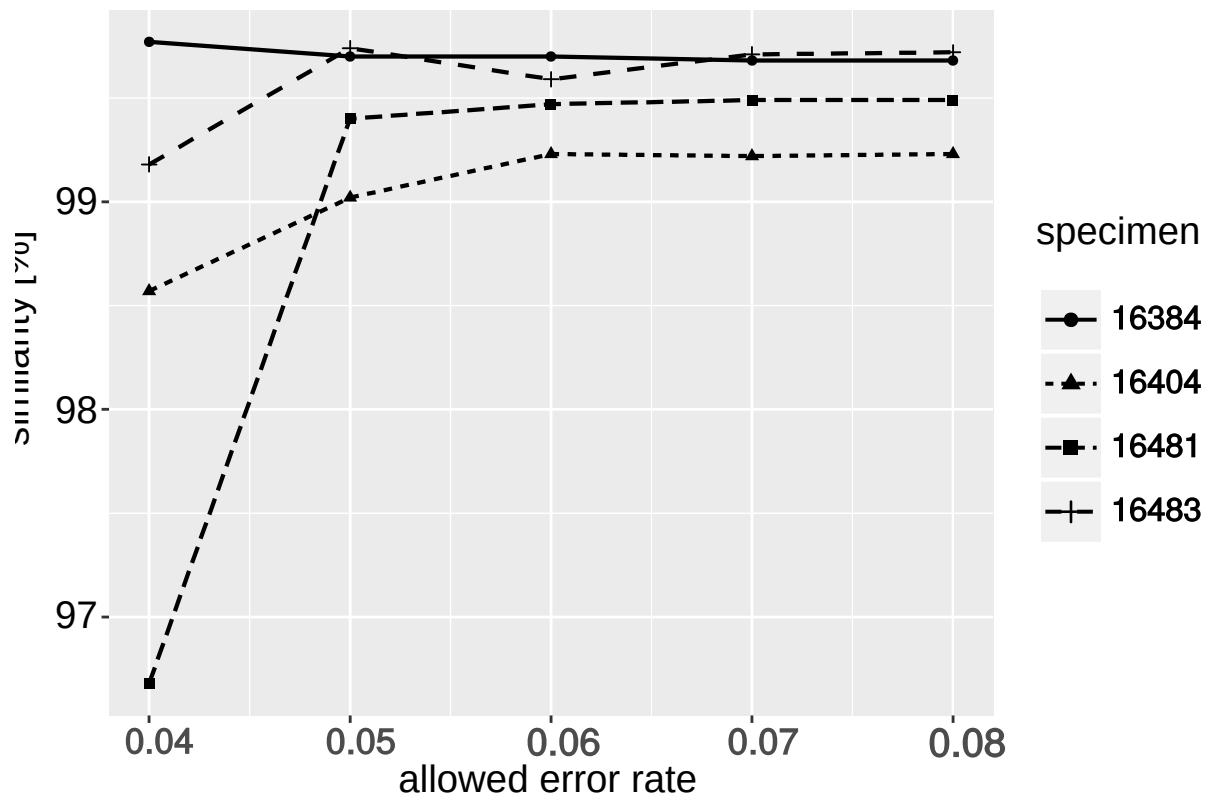

Table S2. Influence of quality filtering on the percentage of passed sequences. The Albacore basecaller already has an internal cutoff of 0.08, which explains the 100% of sequences for 0.08.

specimen	0.04	0.05	0.06	0.07	0.08	total sequences
16384	6.8%	47.7%	79.5%	93.8%	100%	453
16404	3.3%	38.9%	75.8%	90.8%	100%	753
16481	0.8%	21.4%	72.9%	91.1%	100%	594
16483	1.9%	44.2%	79.7%	92.8%	100%	419